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Figure 1

Map of Human CD20/IgE-Receptor Like cDNA (SEQ ID NO: 1) and Amino Acid Sequence (SEQ ID NO: 2) (Agp-96614-a1) (CD20RP2)

1	TTC	CCAC	TGC	TCC	CAGG	CAG	CCI	CAG	CAC	CAAC	AAA	AGA	ACA	TGG	TCT	'AGA	CTG	AAC	TAC	CAA	60
61 1	CTA	LAA	CAT	CTC	CTT	TCA	raa.	TAT	CAC	CCGA	CAC	CAT	CAT M	GGA D	TTC	AAC S	CAC T	CGC A	ACA H	CAG S	120 8
121 9		CGGT V	GTT F		GGT V	'ATT F	TCC P	TCC P	AGA E	raa I	CAC T	TGC A	CTTC S	AGA E	ATA Y	TGA E	GTC S	CAC T	AGA E	ACT L	180 28
181			CAC	'GAC	CTT	TTC		TCA	AAC	:CCC	стт	GCA	AAA	ATI	TTA'	TGC	'TAG	AAA	AAT	GAA	240
29	S	A	Т	T	F	s	Т	Q	S	P	L	Q	K	L	F	A	R	K	M	K	48
241	ΓAA	CTT	'AGG	GAC	TAT	CCA	.GAT	CCI	GTI	TGG	:AA	'TAT	'GAC	CTT	'TTC	TTT:	TGG	AGT	TAT	СТТ	300
49	I	L	G	T	I	Q	I	L	F	G	I	M	T	F	S	F	G	V	I	F	68
301	CCT	TTT	CAC	TTT	GTI	'AAA'	ACC	'ATA	TCC	'AAG	GTI	TCC	CTI	'TAT	'ATT	TCI	TTC	AGG	АТА	TCC	360
69	L	F	Т	L	L	K	P	Y	P	R	F	P	F	I	F	L	s	G	Y	P	88
361	ATT	CTG	GGG	CTC	TGT	'TTT	GTT	'CAT	'TAA	TTC	TGG:	AGC	CTI	CCT	'AA'I	TGC	'AGT	GAA	AAG	AAA	420
89	F	W	G	s	V	L	F	I	N	S	G	A	F	L	I	A	V	K	R	K	108
421	AAC	CAC	'AGA	AAC	TCT	'GAT	AAT	'ATT	'GAG	CCG	AAT	'AA'I	GAA	TTT	TCT	'TAG	TGC	CCT	GGG	AGC	480
109	Т	T	E	Т	L	I	I	L	s	R	I	M	N	F	L	S	A	L	G	A	128
481	raa	AGC	TGG	AAT	CAT	TCT	CCT	CAC	'ATT	TGG	TTT	CAT	CCI	'AGA	TCA	AAA	CTA	CAT	TTG	TGG	540
129	I	A	G	I	I	L	L	T	F	G	F	I	L	D	Q	N	Y	I	С	G	148
541						TAG	TCA	.GTG	TAA	GGC	TGT	TAC	TGT	CCT	GTT	CTT	GGG	AAT	TTT	'GAT	600
149	Y	s	H	Q	N	S	Q	С	K	A	V	T	V	L	F	L	G	I	L	I	168
601	TAC	'ATT	'GAT	GAC	TTT:	CAG	CAT	TAT	TGA	ATT	'ATT	CAT	TTC	TCT	GCC	ттт	CTC	AAT	TTT	'GGG	660
169	Т	L	M	T	F	S	I	Ι	E	L	F	I	s	L	P	F	S	I	L	G	188
661	GTG	CCA	CTC	AGA	GGA	TTG	TGA	TTG	TGA	ACA	ATG	TTG	TTG	ACT	AGC	ACT	GTG	AGA	ATA	AAG	720
189	С	H	s	Е	D	С	D	С	E	Q	С	С	*								201
721	ATG	TGT	'TAA	AAT	CTC	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	A	760						

Figure 2

Map of Human CD20/IgE-receptor Like cDNA (SEQ ID NO: 3) and Amino Acid Sequence (SEQ ID NO: 4) (Agp-69406-a1) (CD20RP1)

1 GGCAGGAACAGCCAGTGGGAGGTTCCAGCTGAGCGCTCCCCAGAGGTGAGCTGATCCCCA GCCACAGCACAGGACCAGGCTGCGAGAACAGCATCATCAGCATCATGCTATTACAATC MLLQS CCAAACCATGGGGGTTTCTCACAGCTTTACACCAAAGGGCATCACTATCCCTCAAAGAGA Q T M G V S H S F T P K G I T I P Q R E GAAACCTGGACACATGTACCAAAACGAAGATTACCTGCAGAACGGGCTGCCAACAGAAAC K P G H M Y Q N E D Y L Q N G L P T E T ${\tt CACCGTTCTTGGGACTGTCCAGATCCTGTGTTGCCTGTTGATTTCAAGTCTGGGGGCCAT}$ TVLGTVQILCCLLISSLGAI CTTGGTTTTTGCTCCCTACCCCTCCCACTTCAATCCAGCAATTTCCACCACTTTGATGTC LVFAPYPSHFNPAISTTLMS TGGGTACCCATTTTTAGGAGCTCTGTGTTTTTGGCATTACTGGATCCCTCTCAATTATCTC G Y P F L G A L C F G I T G S L S I I S TGGAAAACAATCAACTAAGCCCTTTGACCTGAGCAGCTTGACCTCAAATGCAGTGAGTTC G K Q S T K P F D L S S L T S N A V S S ${\tt TGTTACTGCAGGAGCAGGCCTCTTCCTCCTTGCTGACAGCATGGTAGCCCTGAGGACTGC}$ $\begin{smallmatrix} V & T & A & G & A & G & L & F & L & L & A & D & S & M & V & A & L & R & T & A \end{smallmatrix}$ CTCTCAACATTGTGGCTCAGAAATGGATTATCTATCCTCATTGCCTTATTCGGAGTACTA $\verb|SQHCGSEMDYLSSLPYSEYy|$ ${\tt TTATCCAATATATGAAATCAAAGATTGTCTCCTGACCAGTGTCAGTTTAACAGGTGTCCT}$ Y P I Y E I K D C L L T S V S L T G V L ${\tt AGTGGTGATGCTCATCTTCACTGTGCTGGAGCTCTTATTAGCTGCATACAGTTCTGTCTT}$ V V M L I F T V L E L L A A Y S S V F TTGGTGGAAACAGCTCTACTCCAACAACCCTGGGAGTTCATTTTCCTCGACCCAGTCACA W W K Q L Y S N N P G S S F S S T O S O AGATCATATCCAACAGGTCAAAAAGAGTTCTTCACGGTCTTGGATATAAGTAACTCTTGG D H I Q Q V K K S S S R S W I *

CCTCAGAGGAAGGAAAAGCAACTCAACACTCATGGTCAAGTGTGATTAGACTTTCCTGAA

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Figure 3

h TM4	M ··· ASH E	VDNAELG	SASA	HGTPGSET @	EEL - NT S	32
NI GERB	MHOTYSRHOR	PEESTFS	AAMITT NOGNE	CAMPGAGP (U	POLGNM A	44
HURP4 69406	M TSQPV M LL QSQ	FMETII V TMGV SHS	LPS FTP	HVI NE SQAEK KGI TI POREK	PEP PGH	29 29
l qERbot a	MDTESMR	PANLALP	CEPSSVPAF-	EYLEI SPREY	SSGRUL K	40
96614 Htpef86	M DSSTA MYSMISAVPV	HSP~~~VFLV ANSVLVV APH	PPP NG/P/TPGI M	- ET TASEY ES SHVPL VPNSD	TEL - SA T POYHLY FGNP	31 50
h CD2 0	MT TPFM5Y	N	GTF PAEP- MK	GPI AMOSGRK	P LF P-FM	34
HTM4SF5 HTAL6	MOTGKCA MOTGKCA			ROVGL		12
Consonsur	М					12 50
05112 0112 0						90
h TM4	VYHPI NGS	PD-YQKAKLQ	VLGAI"O L NA	AM LALGVIL	GSL QYPYHFQ	79
NIGERS HURP4	VI HSHLWKGL TNOGO: + DSL	OEKFLKGEPK KK-HLHABK	VLGVV A LTA VI GTI A LOG	LMELSME TM MYLSLOE IL	MCMA-SNEYG ASASESPNET	93 76
69406	MY ONE DYL	OH-GLPTETT	VLGTV Q L CC	LLI SSLGAIL	VFAPYP9HFN	76
1 qERbota 96614	SASSPPLHTW	LT-VLKKEGE	FLGVT Q L TA	M CLOFGTW	CSVLDI SHIE	89
HTPEF86	TF STQ SPL PSLVSHVNGQ	OK-LFARHYK PVOKALKEGK	ILGTI DLFG TLGANDIIG	IMFSFGFIF LAH GLGSIM	LFTL-LIPYP ATVL-VŒYL	77 99
PCD50	SSLVG PTO	TFF MRESK	TLGAVO PNS	LFH ALGGIL	-M P-AG YA	78
HTM4SF5 HTAL6	-SLI T	<u>L</u>	OFYCI~VANA ALLCI≩AAN	LLLYPN至 LLYFPN至	-TSWTNF-N -TKY-ASE-N	41 41
Consonsus		E.	. LG. G.L.	LG		100
h TM4	KHFFFFTFYT	GYP1 WGAVFF	CSSGT LSV VA	G KP	T-	114
NIGERB HURP4	SNPLSVY) CV-TSTLLNS	GYTIWGSWYF AYPFIGPFFF	II SOSLSI AA II SOSLSI AT	GIRT EKRL	T-	126 110
69406	PA-1 STTLMS	GYFFL GALCF	GIT (GSLSI15	G005	T-	110
l qERbota 96614	GD-1FSSFKA RFPF1FLS	GYPFWGAIFF GYPFWGSVLF	SISGMLSIIS INSGAFLIAV	KRKT	A-	123
HTPEF86	SI SFYGGF	PF-W-GGLWF	11 SGSLSV AA	ENOP	YS-	110 131
LCD20 HTM4SF5	PI OVTYWY HL SLOVWLMG	PL-W GGIMY GF-I GGGLMV	II SESULAAT	EK/15	CGN RC	109
HTAL6	HL SPFVWFFS	GI - VGGSLLM	Lorgiawita Llpatyfigl	GGRGCCGAGC EGDCCC GC	COMENCOKRO	85 88
Consensus		G7GF	.15G LSI			150
h TM4 higerb		KGL	I ONSTONEA VRGSLOMET	SATI ALVOJA SSVLAASGIL	FLSLN AVN	147
HURP4		KLL	VHSSL VGS1L	SALSALVGR	INTFSLÆFY- ILSVKRÆFLNI	158 143
69406		KPF	DLSSLT91AV	SSYTAGAGLE	LLADSMALR	143
1 qERbeta 96614		TYL	VRGSLGWJA I I LSRIMIFL	SSI AGGTG[T SALGAI AGI]	ILIINLIKKSL Lltf@fildo:	156 143
HTPEF86		YCL	LSGŞLGLN∯V	SAI CSAVGVI	LFI TOLS	161
NCD20 HTM4SF5	RMLRSVF SSA	FGYLGAI YCL	YKGRMIMISL SYSGAGLRNG	SLFAAI 9GN FROLMN-GEW	LSI MOI UNI K GYHFE• •• • D	142 130
HTAL 6	AMLSSVL AAL	I GI AGSGYOV	I VAAL GLAEG	PLOLDSLGOW	NYTFAS	134
Cansons w		L	SEGNÂ	Š A G		200
NTM4 NIGERB	QSLRSCHSSS -SFH-H	E SPILC	NYMGSI	SH	- GMPSLL-LI	179
NIGERB HURP4	-SFHH PASLOCELDK	P-YC N-NI PTRSYV	NYY GNS SYFYHDSLYT	NHCHGTMGIL TOCYTAKASL	MGL.DGM()- LL AGT LSLM LI	190 191
NIGERB Hurpa 69406	-SFH-H PASLOCELDK TASOHOGSEM	P-YC N-NI PTRSYV D-YLSSL PYS	NYY GNS SYF YHDSL YT EYY YP-I YEI	NNCHSTMSIL TOCYTAKASL KOOLL TSVSL	MGL DGM(+ LL AGT LSLM LI TGV LVV M LI	190 191 190
higere HURP4 69406 igerbota 96614	-SFH-H PASLOCE LDK TASCHOGSEM AYI H	P-YC N-M PTRS/V D-YLSSLP/S	NYY GNS SYF YHDSL YT EYY YP-1 YEI KFFE GYSHQN	NNCHGTMGIL TDCYT AKASL KDOLL TSVSL TKOFMASF S SOCKA	MGL.DGM()- LL AGT LSLM LI	190 191
NI GERB HURP4 69406 I gERbota 96614 HTPEF86	PASLOCE LOK TASCHOGSEM AVIH NVI	P-YC N-NI PTRS/V D-YLSSL PYS I H500 C PY A/P	N7Y GNS S7F YHDGL YT EYY YP-1 YEI KFFE G7SHQN DYY	NNCHGTMS/L TDCYT AKASL KOCLL TS/SL TKOFMASF S SOCKA	MSL DGM/- LL AGT LSL M LI TG/ LQV M LI TEI VVMM LF VTV LFL G I L AWGVNPG MA	190 191 190 187 167 183
NIGERS HURP4 69406 I qERbata 96614 HUPEF86 NCD20 HUMISF5	PASLOCE LDK TASCHOGSEM AVIH NYI I SHFLKMESL TAG	P-YC N-M PTRS/V D-YLSSLP/S	NYY GHS SYF YHDSL YT EYY YP-I YEI KFFE GYSHQN DYY NI YHCEPANP RCE	NNCHGTMGIL TDCYT AKASL KDOLL TSVSL TKOFMASF S SOCKA	MGL DGM/- LL AGT LSL M LI TGV LQV M LI TEI VVMM-LF VTV LFL G I L	190 191 190 187 167
NI GERB HURPA 69406 I GERbata 96614 HIPEF86 NODEO HIMASF5 HTAL6	- SFH-H	P-YC N-M PTRS/V D-YLSSLP/S	NY GHS SYF YHOSL YT EYY YP-1 YE! KFFE GYSH2N DYY NI Y NOEPANP RCE ECT	NHOHETIMEIL TOOYT AKASL KOOLL TSVSL TKOFMASF S SOCKA PY SEINISPST OV	MSL DOMP- LL AGT LSL M LI TGY LSV M LI TEI VVMM LF VTV LFL G I L ANGVIPPG MA CYSI QSLFLG	190 191 190 187 167 183 192 157
NIGERS HURP4 69406 I qERbata 96614 HUPEF86 NCD20 HUMISF5	PASLOCE LDK TASCHOGSEM AVIH NYI I SHFLKMESL TAG	P-YC N-MI PTR S/V D-YLS SL P/S	NYY GHS SYF YHDSL YT EYY YP-I YEI KFFE GYSHQN DYY NI YHCEPANP RCE	NNCHGTMEIL TDOYT AKASL KOOLL TSYSL TKOFMASF S SOCKA	MGL DGM/- LL AGT LSL M LI TGV LVV M LI TEI VVMM LF VTV LFL G I AMGVPP G MA CYSI CSLIF LG PRV VPWN VT	190 191 190 187 167 183 192
NI GERB HURPA 69406 I qERbota 98614 HIPEF86 NCD20 HIPMSP5 HTAL6 Consense	-SFH-H- PASLOXELDK TASCHOSSEM AVIH NYI I SHFLKMESL TAG TEG	P-YC N-M PTR 3/V D-YLSSL P/S	NIY GHS SYF YHDS. YT KFFE GISHQN DYYN N Y NOEPANP PCE ECT	NNCHSTMEIL TDOYT AKASL KDOLL TSY SL TKOFMASE S SOCKA	ME DOMP-LL AGT LSL M LI TGY LOV M LI TEI VUMM LF VAUFLE G I L AUGUNP G MA CVSI QSLF LG PRO VPWN VT ICH VEWN VS	190 191 190 187 167 183 192 157 161
higers HURP4 69406 1 geRheta 96614 HTPER6 60020 HTM S75 HTML Component	-SFH-H	P-YC N-N PTRSY D-YLSSLPYS	NYY GHS SYF YHOSL YT EYY YP-1 YE IVFE GYSHQN DYYN N Y NOEPANP RCEY	NICHSTMEIL TOOYT AKAS. KOOLL TSV S. TKCFMASF S. SXCKA SENISPST OF SENISPS	ME DOMP- LL AGT LSL M LI TGY LOV M LI TEI WWM LF TYP LF L G I L AMSVPP G MA CYSI CSLF LG PRV VPNN VT ICH VEWN VS	190 191 190 187 167 183 192 157
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NI GERS HURP4 69406 I qERbata 986614 HIPER86 NCD20 HIMISTS HTAL6 Consideration NIMISTS HURP4 69406 I qERbata 96614	-SFH-H PASLOGE LDK TASCHOG SEM ANTH		NYY GHS SYF YHDS. YT EYY YP-1 YE KFFE GYSK0E N Y NOEPANP ROE ECT	NOGETHELL TOOTH ANAL KOOLL 1579.1 TKOTMAST S SOCKA	MGL DGMP-LL MGL DGMP-LL MGL LYVM-M LI TGP LYVM-M LI TGP LYVM-M LI TGP LYVM-M MGL TGP LI MAGNIPG-MA MGL TGP MGL	190 191 190 187 167 183 192 157 161 250 203 224 226 224 222
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NIGERS HURP4 69406 1 4ERbeta 96614 HTPET86 HOD20 HTMGF5 HTML STM NIGERS HURP4 69406 1 4ERbeta 96614 HTPET86 HOD20 HTMGF5 HTMLSF5 HTML655 HTMLSF5 HTML655 HTMLSF5 HTMLS	-SFH-H PASLOCE LDK TASCHOS SEM AN IH NII NII NII		NYY GNS SYF YHOEL, YT EYY YP-I YEI GYF	NNGSTHEIL TOOTI AGAS. KOOLL TSYS. TICKTMGFT S SOCKA	MEL DRAW LLI TGRILVYM MLI TGRILVYM MLI TGRILVYM MLI TGRILVYM MLI TGRILVYM MLI VITVIFI.G I IL AUGUNPE I MA O'FSI OSIFI.G FRW VPAN VI L GGR VLI LPSH GGR VLI LPSH GGSVIFI.HSY GSSFSS TOS — ——————————————————————————————————	190 191 190 187 167 183 192 157 161 250 203 224 226 227 247 242 190 217 242 186
NI GERB HURPH 69406 I GERBEET 1 GERBEET HTMLST5 HTML6 COMMAN OF LIGERB HURPH 69406 I GERBET HTPERS6 LOCO20 HTMST5 HTML575 HTML575 HTML575 HTML575 HTML575 HTML575 HTML575 HTML575 HTML575	-SFH-H PASLOCE LDK TASCHOGSEM ANI H NI ISHELMESL TAG TE G LTILLELOVII LSWLEFCI AW COLLEFCI AW COLLEFCI AW TILLEGESAW LTILLELSSAW LTIL		NYYGHS SYFYHELS-S SYFYHELS-S SYFYHELS-S EVENN DYY	NOGSTHEIL TOYT AGES. KOOLL 159 S. TKOTMAGE S. SOOKGA	MG. DGMP-LL AGG LGWM LI TGY LGWM LI TEI WWM LI AGG LGWM TO SI GO WLI	190 191 190 187 167 167 169 250 203 224 226 224 222 217 242
NIGERS HURP4 69406 1 4ERbeta 96614 HTPET86 HOD20 HTMGF5 HTML STM NIGERS HURP4 69406 1 4ERbeta 96614 HTPET86 HOD20 HTMGF5 HTMLSF5 HTML655 HTMLSF5 HTML655 HTMLSF5 HTMLS	-SFH-H PASLOCE LDK TASCHOS SEM AN IH NII NII NII		NYY GNS SYF YHOEL, YT EYY YP-I YEI GYF	NNGSTHEIL TOOTI AGAS. KOOLL TSYS. TICKTMGFT S SOCKA	MEL DRAW LLI TGRILVYM MLI TGRILVYM MLI TGRILVYM MLI TGRILVYM MLI TGRILVYM MLI VITVIFI.G I IL AUGUNPE I MA O'FSI OSIFI.G FRW VPAN VI L GGR VLI LPSH GGR VLI LPSH GGSVIFI.HSY GSSFSS TOS — ——————————————————————————————————	190 191 190 187 183 192 157 161 250 203 224 222 24 222 186 300
NI GERS HURPH 69406 I qERbeta 996614 HIPERS 60020 HIMISTS HIALE Consons w NIMM 61GERS HURPA 69406 I qERbeta 96614 HIPERS 60020 HIMISTS HIALE Consons w NIMM 69406 Consons w NIMM 69406 I qERbeta 96614 HIPERS 6020 HIMISTS HIALE Consons w NIMM 6020 HIMISTS	-SFH-H PASLOGE LDK TASCHOG SEM ANTH NTI ISPILINGS. TAG TE G LTILLELOVTI LSVLEFCI AV COLLEFOL AV TILLEGOM LTILLIG.GSAW LTILLIG.GSAW LTILLIG.GSAW LTILLIG.GSAW LSVLLYFG.		NYY GHS SYF YHOLE, S SYF YHO	NNSTHEIL TOYT AGAS. KOCLL TSYS. TICKTMAST S SOCKA	MS. DGMP-LL MG LGWM-LL TGP LGWM-LL TET WHM-LF TET WHM-LF TET WHM-LF TET WHM-LF GI-L AMGHP-G-MA GIST LG FRW UPWM-VI L GGWVLI LP-SH GGWVL	190 191 190 187 183 157 161 250 203 224 226 227 227 247 247 248 250 217 248 250 217 248 250 217 248 250 261 272 273 274 275 275 275 275 275 275 275 275 275 275
AIGERS HURP4 59406 19614 19614 HIPE78 6D20 HIPM ST5 HTML ST6 AIMM AIGERS HURP4 69406 19ER5 19ER5 19ER5 HIPE786 6CD20 HIPM ST5 HIPE786 COD20 HIPM ST5 HIMESF5 HIMESF5 HIMESF6 COD20 AIMM AIGERS AIMM AIMM AIGERS AIMM AIGERS AIMM AIGERS AIMM AIGERS AIMM AIGERS AIMM AIMM AIGERS AIMM AIGE	-SFH-H PASLOCE LDK TASCHOS EM AVI H VI I LT LLELOVII LSVLEFCI AV FI VLELLLAA TITLG LSSAW ITLNIFS II VI SGULLYFG LL SMLI FAF LI SLLVAASC LF SLVAASC		NYY GNS SYF YHOLS, YT SYY YP-1 YE SYF YHOLS, YT SYY YP-1 YE SYSH2N DYY	NNSTHEIL TOYT AGAS. KOOLL TSYS. TKOPHAGE S T	MEL DRAW LLI TGRILVUM LLI TGRILVUM LLI TGRILVUM LLI TGRILVUM LLI VITULFILG I IL ANGENPE MA VENNA VE TGRILVUM	190 191 191 187 183 157 161 250 203 224 226 222 190 242 186 300 214 234
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